

**PROCEEDINGS OF
THE 2011 INTERNATIONAL CONFERENCE ON
BIOINFORMATICS & COMPUTATIONAL BIOLOGY**

BIOCOMP 2011

Volume II

Editors

**Hamid R. Arabnia
Quoc-Nam Tran**

Associate Editors

**Matthew He, Andy Marsh
Ashu M. G. Solo
Jack Y. Yang**



WORLDCOMP'11

July 18-21, 2011

Las Vegas Nevada, USA

www.world-academy-of-science.org

©CSREA Press

This set of volumes contain papers presented at The 2011 International Conference on Bioinformatics & Computational Biology (BIOCOMP'11). Their inclusion in this publication does not necessarily constitute endorsements by editors or by the publisher.

Copyright and Reprint Permission

Copying without a fee is permitted provided that the copies are not made or distributed for direct commercial advantage, and credit to source is given. Abstracting is permitted with credit to the source. Please contact the publisher for other copying, reprint, or republication permission.

Copyright © 2011 CSREA Press
ISBN: 1-60132-170-8, 1-60132-171-6 (1-60132-172-4)
Printed in the United States of America

CSREA Press
U. S. A.

Foreword

It gives us great pleasure to introduce this collection of papers to be presented at the 2011 International Conference on Bioinformatics and Computational Biology (BIOCOMP'11), July 18 through 21, 2011, at Monte Carlo Resort, Las Vegas, USA.

The Academic Co-Sponsors of this year's conference include:

The Berkeley Initiative in Soft Computing (BISC), University of California, Berkeley, USA; Biomedical Cybernetics Laboratory, HST of Harvard University and Massachusetts Institute of Technology (MIT), USA; Intelligent Data Exploration and Analysis Laboratory, University of Texas at Austin, Austin, Texas, USA; Collaboratory for Advanced Computing and Simulations (CACs), University of Southern California, USA; Minnesota Supercomputing Institute, University of Minnesota, USA; Knowledge Management & Intelligent System Center (KMIS) of University of Siegen, Germany; UMIT, Institute of Bioinformatics and Translational Research, Austria; BioMedical Informatics & Bio-Imaging Laboratory, Georgia Institute of Technology and Emory University, Atlanta, Georgia, USA; Hawkeye Radiology Informatics, Department of Radiology, College of Medicine, University of Iowa, Iowa, USA; NDSU-CIIT Green Computing and Communications Laboratory, USA; Supercomputer Software Department (SSD), Institute of Computational Mathematics & Mathematical Geophysics, Russian Academy of Sciences, Russia; SECLAB (inter-university research groups at University of Naples Federico II, the University of Naples Parthenope, and Second University of Naples, Italy); Medical Image HPC & Informatics Lab (MiHi Lab), University of Iowa, Iowa, USA; Intelligent Cyberspace Engineering Lab., ICEL, Texas A&M University (Com./Texas), USA; and Model-Based Engineering Laboratory, University of North Dakota, North Dakota, USA.

Corporate Co-Sponsors, Co-Sponsors At-Large and Organizers include:

A number of university faculty members and their staff (names appear below and also on the cover of the proceedings); World Academy of Science (www.world-academy-of-science.org/); Computer Science Research, Education, and Applications Press; High Performance Computing for Nanotechnology (HPCNano); International Society of Intelligent Biological Medicine; World Academy of Biomedical Sciences and Technologies; The International Council on Medical and Care Computetics; The UK Department for Business, Enterprise & Regulatory Reform, UK; and Scientific Technologies Corporation; HoIP - Health without Boundaries. In addition, several publishers of computer science and computer engineering books and journals, chapters and/or task forces of computer science associations/organizations from 8 countries, and developers of high-performance machines and systems provided significant help in organizing the conference as well as providing some resources.

An important mission of WORLDCOMP (a federated congress to which this conference is affiliated with) includes "Providing a unique platform for a diverse community of constituents composed of scholars, researchers, developers, educators, and practitioners. The Congress makes concerted effort to reach out to participants affiliated with diverse entities (such as: universities, institutions, corporations, government agencies, and research centers/labs) from all over the world. The congress also attempts to connect participants from institutions that have **teaching** as their main mission with those who are affiliated with institutions that have **research** as their main mission. The congress uses a quota system to achieve its institution and geography diversity objectives."

The program committee would like to thank all those who submitted papers for consideration. About 44% of the submissions were from outside the United States. Each paper was peer-reviewed by two experts in the field for originality, significance, clarity, impact, and soundness. In cases of contradictory recommendations, a member of the conference program committee was charged to make the final decision; often, this involved seeking help from additional referees by using a double-blinded review process. In addition, papers whose authors included a member of the conference program committee were evaluated using the double-blinded review process. The only exception to the above evaluation process was for papers that were submitted directly to chairs/organizers of approved sessions/workshops; in these cases, the chairs/organizers were responsible for the evaluation of such submissions. The overall paper acceptance rate for regular papers was 24%; 12% of the remaining papers were accepted as poster papers.

We are very grateful to the many colleagues who helped in organizing the conference. In particular, we would like to thank the members of the BIOCAMP'11 Program Committee who we hope will offer their help again in organizing the next year's conference (BIOCAMP'12). The BIOCAMP'11 Program Committee members were:

- *Dr. Selim Aissi, (Steering Committee - WORLDCOMP), Chief Strategist - Security, Manageability and Virtualization, Ultra Mobile Group, Intel Corporation, USA*
- *Prof. Fadhil M. Al-Akwaa, Biomedical Engineering Department, University of Science & Technology, Sana'a, Yemen*
- *Prof. Hamid R. Arabnia, (Steering Committee - WORLDCOMP), Elected Fellow, ISIBM; Editor-in-Chief, The Journal of Supercomputing; Advisory Board, IEEE TC on Scalable Computing; University of Georgia, Georgia, USA*
- *Prof. Ruzena Bajcsy (Steering Committee - WORLDCOMP), Member, National Academy of Engineering; IEEE Fellow; ACM Fellow; University of California, Berkeley, California, USA*
- *Dr. Elhadj Benkhelifa, Senior Research Fellow, Staffordshire University, UK*
- *Prof. H-P. Bischof, Rochester Institute of Technology, Rochester, New York, USA*
- *Prof. Hong Cai, University of Texas at San Antonio, San Antonio, Texas, USA*
- *Dr. Rui Chang, University of California, San Diego, California, USA*
- *Dr. Junaïd Chaudhry, University of Hail, Hail City, Saudi Arabia*
- *Dr. Long Chen, Senior Engineer, Qualcomm Incorporated, San Diego, California, USA*
- *Prof. Art Cho, Chairman of the Department of Biotechnology and Bioinformatics, Korea University, Korea*
- *Prof. Hyunseung Choo, (Steering Committee - WORLDCOMP), ITRC Director of Ministry of Information and Communication; Director, Korea Information Processing Society; Associate Editor, ACM Transactions on Internet Technology; Sungkyunkwan University (SKKU), Korea*
- *Prof. Ping-Tsai Chung, Chair, Computer Science Department, Long Island University, Brooklyn, New York, USA*
- *Prof. Kevin Daimi, Director, Computer Science and Software Engineering Programs, University of Detroit Mercy, Detroit, Michigan, USA*
- *Prof. Youping Deng, Director of Cancer Bioinformatics, Rush University Cancer Center, Rush University Medical Center, Chicago, Illinois, USA*
- *Dr. Mohsen Doroodchi, Cardinal Stritch University, Milwaukee, Wisconsin, USA*
- *Prof. (Winston) Wai-Chi Fang, (Steering Committee - WORLDCOMP), IEEE Fellow; Director, System-on-Chip Research Center; TSMC Distinguished Chair Professor; National Chiao Tung University, Hsinchu, Taiwan*
- *Dr. Haishan Gong, eBay Inc., Sunnyvale, California, USA*
- *Prof. George A. Gravvanis, Democritus University of Thrace, Greece*
- *Dr. Dongfeng Han, University of Iowa, Iowa City, Iowa, USA*
- *Prof. Ray R. Hashemi, Yamacraw Professor of Computer Science, Armstrong Atlantic State University, Savannah, Georgia, USA*
- *Prof. Matthew He, Director, Division of Math, Science, & Technology, Nova Southeastern University, Ft. Lauderdale, Florida, USA*
- *Prof. Xiangjian (Sean) He, Director of Intelligent Image Processing and Computer Vision; Deputy Director of Research Centre for Innovation in IT Services and Applications (iNEXT); University of Technology, Sydney, Australia*
- *Prof. Kun Chang Lee, (Steering Committee - WORLDCOMP), Professor of MIS and WCU Professor of Creativity Science, Sungkyunkwan University, Seoul, South Korea*
- *Prof. Simon Lin, Director of Bioinformatics, Center for Cancer Nanotechnology Excellence, Northwestern University, Chicago, Illinois, USA*
- *Dr. Shaoshan Liu, Microsoft, one Microsoft Way, Redmond, Washington, USA*
- *Dr. Yan Luo, National Institute of Standards and Technology (NIST), Maryland, USA*
- *Dr. Reza Malekian, Head, Computer Division, Azad University, Tonekabon, Iran*
- *Prof. Andy Marsh, (Steering Committee - WORLDCOMP), Director HoIP; Director HoIP Telecom, UK; Secretary-General WABT; Vice-president ICET; Visiting Professor University of Westminster, UK*
- *Dr. Ali Masoudi-Nejad, PI, Laboratory of Systems Biology and Bioinformatics (LBB) & Head of the Department of Bioinformatics, University of Tehran, Iran*
- *Sara Moein, Faculty of Engineering, Multimedia University, Malaysia*
- *Dr. Armin Mehran, Islamic Azad University, Tehran, Iran*
- *Dr. Nitin, Distinguished Adjunct Professor, University of Nebraska at Omaha, Omaha, Nebraska, USA*

- *Dr. R. Ponalagusamy, Professor and Head, Department of Mathematics, National Institute of Technology, Tiruchirappalli, India*
- *Prof. Junfeng Qu, Clayton State University, Morrow, Georgia, USA*
- *Prof. Kishore R. Sakharkar, Infectious Disease Cluster, Advanced Medical & Dental Institute (AMDI), University Sains Malaysia, Malaysia*
- *Dr. Akash Singh, IBM, Sacramento, California, USA*
- *Dr. Brajesh Kumar Singh, Reader, Department of C.S.E, FET, RBS College, Bichpuri, India*
- *Prof. R. K. Singh, Uttarakhand Technical University, Dehradun, Uttarakhand, India*
- *Sunil Kr. Singh, Uttarakhand Technical University, Dehradun, Uttarakhand, India*
- *Ashu M. G. Solo, (WORLDCOMP Publicity Chair), Fellow of British Computer Society, Principal/R&D Engineer, Maverick Technologies America Inc.*
- *Dr. Jie Tang, University of California Irvine, California, USA*
- *Prof. Dr. Qurat-ul-Ain Tariq, Chairperson, Department of Computer and Information Systems Engineering, NED University of Engineering & Technology, Karachi, Pakistan*
- *Prof. Quoc-Nam Tran, (Vice-Chair, BIOCAMP), Lamar University, Beaumont, Texas, USA*
- *Dr. Vladimir Volkov, The Bonch-Bruевич State University of Telecommunications, Saint-Petersburg, Russia*
- *Dr. Guanghui Wang, Department of Systems Design, University of Waterloo, Canada*
- *Dr. Xuewei Wang, Michigan State University, East Lansing, Michigan, USA*
- *Prof. Yufeng Wang, University of Texas at San Antonio, Texas, USA and South Texas Center for Emerging Infectious Diseases, San Antonio, Texas, USA*
- *Prof. Layne T. Watson, (Steering Committee - WORLDCOMP), IEEE Fellow; NIA Fellow; ISIBM Fellow; Fellow of The National Institute of Aerospace; Virginia Polytechnic Institute & State University, Virginia, USA*
- *Prof. Jongwook Woo, President, KSEA-SC; Director of HiPiC; California State University, Los Angeles, California, USA*
- *Dr. Jack Y. Yang, Harvard University, USA & Board of Directors of ISIBM & Editor-in-Chief, Int'l Journal of Functional Informatics and Personalized Medicine, USA*
- *Prof. Lotfi A. Zadeh, (Steering Committee - WORLDCOMP), Member, National Academy of Engineering; IEEE Fellow, ACM Fellow; AAAS Fellow; AAAI Fellow; IFSA Fellow; Director, BISC; University of California, Berkeley, California, USA*
- *Hao Zheng, Georgia Institute of Technology, Georgia, USA*
- *Dr. Songfeng (Andy) Zheng, Missouri State University, Springfield, Missouri, USA*

We express our gratitude to keynote and invited speakers of WORLDCOMP and individual conference/tracks and tutorial speakers - the list of speakers appears on the conference web site.

We would also like to thank the followings: UCMSS (Universal Conference Management Systems & Support, California, USA) for managing all aspects of the conference; Dr. Tim Field of APC for managing the printing of the proceedings; and the staff of Monte Carlo Resort in Las Vegas for the professional service they provided. Last but not least, we would like to thank the Associate Editors of BIOCAMP 2011: Drs. Matthew He, Andy Marsh, Ashu M. G. Solo, and Jack Y. Yang.

We present the proceedings of BIOCAMP'11.

Hamid R. Arabnia and Quoc-Nam Tran

General Co-Chairs/Vice-Chairs & Coordinators, BIOCAMP'11

Contents

SESSION: COMPUTATIONAL METHODS FOR MICROARRAY, GENE EXPRESSION ANALYSIS, AND GENE REGULATORY NETWORKS

Optimization of a Microarray Probe Design Focusing on the Minimization of Cross-hybridization	3
<i>Fabian Horn, Hans-Wilhelm Nutzmann, Volker Schroeckh, Reinhard Guthke, Christian Hummert</i>	
EMMA: An EM-based Imputation Technique for Handling Missing Sample-Values in Microarray Expression Profiles.	10
<i>Amitava Karmaker, Edward Salinas, Stephen Kwek</i>	
Creation and Comparison of Different Chip Definition Files for Affymetrix Microarrays	16
<i>Christian Hummert, Franziska Mech, Fabian Horn, Michael Weber, Susanne Drynda, Ulrike Gausmann, Reinhard Guthke</i>	
A Validation Method for Fuzzy Clustering of Gene Expression Data	23
<i>Thanh Le, Katheleen Gardiner</i>	
Robust SVD Method for Missing Value Estimation of DNA Microarrays	30
<i>Fen Qin, Joseph Collins, Jeonghwa Lee</i>	
Finding Biomarkers for Non-Small Cell Lung Cancer Diagnosis with Novel Data Mining Techniques	36
<i>Quoc-Nam Tran</i>	
Identification of Pseudo-Periodic Gene Expression Profiles	42
<i>Li-Ping Tian, Li-Zhi Liu, Fang-Xiang Wu</i>	
Gene Selection using Multidimensional False Discovery Rate	47
<i>Ahmed Moussa, Mounir Maouene, Brigitte Vannier</i>	
Letting all have a say - A novel method for microRNA RT-PCR normalization	52
<i>Rehman Qureshi, Ahmet Sacan</i>	
Classification of High-throughput Data Using Correlation-shared Gene Clusters	58
<i>Pingzhao Hu, Hui Jiang</i>	
Markov Model Checking of Probabilistic Boolean Networks Representations of Genes	63
<i>Marie Lluberes, Jaime Seguel, Jaime Ramirez-Vick</i>	

Reliability Analysis of Classification of Gene Expression Data 69
Sujata Dash, Bichitra Nanda Patra

**SESSION: BIOINFORMATICS DATABASE, DATAMINING, AND PATTERN
DISCOVERY TECHNIQUES**

Clustering on Protein Sequence Motifs using SCAN and Positional Association Rule Algorithms 79
Bernard Chen, Ben Nordin, Sriram Bobba, Devendar Singireddy, Brad Taylor, Sinan Kockara, Mutlu Mete

Constructing Super Rule Tree (SRT) for Protein Motif Clusters Using DBSCAN 85
Bernard Chen, Sait Suer, Muhyeddin Ercan, Rahul Tada, Recep Avci, Sinan Kockara

Mapping Genes to Diseases With Translational Data Mining 91
Modest Von Korff, Axel Klenk, Thomas Sander

Protein Sequence Motif Extraction Using Decision Forest 96
Bernard Chen, Cody Hudson, Minwoo Kim, Aaron Crawford, John Wright, Dongsheng Che

Matlab Toolbox for Data Reduction, Visualization, Classification and Knowledge Extraction of Complex Biological Data 103
Ali Mohammad-Djafari, Ghazaleh Khodabandelou, Jerome Lapuyade-Lahorgue

Portable Measurement System of the Spasticity Based on the K-means Clustering Algorithm of the Tonic Stretch Reflex Threshold 110
Chul-Gyu Song, Keo-Sik Kim, Min-Ho Kim, Sang-Hun Ryu

GPU Accelerated PK-means Algorithm for Gene Clustering 116
Wuchao Situ, Yau King Lam, Yi Xiao, Peter Wai Ming Tsang, Chi Sing Leung

Computation of Coronary Sinus Pressure Using Pattern Recognition Techniques 121
Loay Alzubaidi, Ammar El Hassan, Jaafar Al Ghazo

Linear Models and Biomarker Search with Microarray Data 126
Eulisa Rivera, Matilde Sanchez-Pena, Clara Isaza, Jaime Seguel, Mauricio Cabrera-Rios

Comparative Analysis of Krylov Iterative Methods in Support Vector Machines 131
Matthew Freed, Joseph Collins, Jeonghwa Lee

Fast Splice Site Classification Using Support Vector Machines in Imbalanced Data-sets 136
Jair Cervantes, Asdrubal Lopez Chau, Adrian Trueba Espinoza, Jose Sergio Ruiz Castilla

A Study on Acupressure Points Online Database 142
Zizhong Wang, Tara Santos

Human Identification via Neural Network 148
Parviz Eshaghi

Telomerase Gene Prediction Using Support Vector Machines 152
David Luper, Spandana Makeneni

**SESSION: PROTEIN CLASSIFICATION + STRUCTURE PREDICTION,
EVOLUTIONARY, AND COMPUTATIONAL MOLECULAR + STRUCTURAL
BIOLOGY**

Solving Planted Motif Problem Using Modeling Method 161
Subramanyam Desaraju, Ravi Mukkamala

Predicting Sequence and Structural Specificities of RNA Binding Regions Recognized by Splicing Factor SRSF1 168
Xin Wang, Liran Juan, Junjie Lv, Kejun Wang, Jeremy Sanford, Yunlong Liu

Correlation of Patristic Distance with Nominal Specimen Collection Date in Influenza A/H1N1 Hemagglutinin-Encoding Segments 175
Jack Horner

Identification of Transcriptional Regulatory Elements by Functional Enrichment Analysis. 182
Amitava Karmaker, Stephen Kwek

An Integrated Pipeline for Protein Classification using Specific PSSMs and Existing Protein Annotations 188
Kyung Dae Ko, Hongfang Liu

Predicting DNA-Binding Sites by Exploring the Distribution of Atom Groups around the Surface 192
Jing Hu, Changhui Yan

Structural Analysis of Molecular Networks: AMES Mutagenicity 196
Laurin AJ Mueller, Karl G Kugler, Matthias Dehmer

A Study of Correlations Between the Definition and Application of the Gene Ontology 202
Yuji Mo, Catherine Anderson, Stephen Scott

Phylogenetic Analysis Workflow Using the BioExtract Server 209
Yosr Bouhlal, Douglas Jennewein, Carol Lushbough

SESSION: COMPARATIVE SEQUENCE, GENOME ANALYSIS, GENOME ASSEMBLY, AND GENOME SCALE COMPUTATIONAL METHODS

A Regression-based Approach for Estimating Recombination Rate from Population Genomic Data 215

Lan Zhu, Feng Feng, Carlos Bustemante

Evaluation of the Suitability of a Zipfian Gap Model for Pairwise Sequence Alignment 222

Ramu Chenna, Toby Gibson

A Probabilistic Approach for Characterizing the Marking System of Multiplex Sequencing in ABI SOLiD Platform 228

Fabio Lobato, Pericles Machado, André Goncalves, Andrea Ribeiro-dos-Santos, Dayse Alencar, Sylvain Darnet, Adamo Santana

Enhancement on the Predictive Power of the Prediction Model for Human Genomic DNA Methylation 232

Hao Zheng, Shi-Wen Jiang, Hongwei Wu

Parallelization of Needleman-Wunsch String Alignment Method 239

Jaime Seguel, Carlos Torres

Genetic Matching: An Efficient Algorithm to Adjust Covariate Imbalance for Data Analysis and Modeling 245

Kao-Tai Tsai, Karl Peace

A CAM (Content Addressable Memory)-based Architecture for Molecular Sequence Matching 252

Parag Lala, James Parkerson

Effective Algorithms for Altering Human Chromosome Shapes 257

Wei Wu, Xiaoli Yang, Charles Tseng

Identification of Minimum Redundancy Tagging SNPs via Gibbs Sampling 262

Gaolin Zheng

Development Approach and Architecture of GenSAS : the Genome Sequence Annotation Server 267

Taein Lee, Il-Hyung Cho, Cameron Peace, Sook Jung, Ping Zheng, Doreen Main

Sequence Analysis to Predict Protein Active Sites using SSHM 274

Satheesh Patchikolla, Srinivas Bagam, Prasada Mandala, Appa Rao Allam, Charles Babu Gundupalli

**SESSION: COMPUTATIONAL METHODS FOR FILTERING, NOISE
CANCELLATION, AND SIGNAL + IMAGE PROCESSING**

**Quantifying Phenotypic Traits in Retinal Coronary Angiography: Automated Extraction of
Retinal Vasular Networks and Localization of Optic Discs in Fundus Images** 279

Hesam Dashti, James Driver, Nader Sheibani, Amir Assadi

**Common-Path Fourier-Domain Optical Coherence Tomography using Surface Tracking
Algorithm** 285

Chul-Gyu Song, K. S. Kim, M. H. Kim, Sang-Hun Ryu, J. H. Seo

Registration of Confocal Fluorescence Endomicroscopy Images Using Phase Correlation 291

Feng Zhao, T. M. McGinnity

Signal Processing Algorithm for Wireless ECG Monitoring Systems 297

Abishek Thekkeyil Kunnath, Sahajhaksh Hariharan, Maneesha Vinodini Ramesh

**Tracking of Active Cells Based on Kalman Filter in Time Lapse of Image Sequences of
Neuron Stem Cells** 301

Chunming Tang, Yanqing Wang, Ying Cui

**An Efficient Soft Graph Clustering Method for PPI Networks based on Purifying and
Filtering the Coupling Matrix** 307

Ying Liu, Amir Foroushani

BRATUMASS Antenna Positioning Optimization with Genetic Algorithm 311

Zhongling Han, Zhifu Tao, Meng Yao, Yizhou Yao, Blair Fleet, Erik D. Goodman, John R. Deller

Application of Quarter Iteration of FRFT in BRATUMASS for Weak Signal Extraction 315

Zhongling Han, Zhifu Tao, Meng Yao, Yizhou Yao, Blair Fleet, Erik D. Goodman, John R. Deller

An X-Ray On Methods Aiming At Arrhythmia Classification In ECG Signals 319

Eduardo Luz, David Menotti

**The Application of the Genetic Algorithm Tool Box at Target Enhancement Processing in
Breast Cancer Microwave Imaging** 325

Zhongling Han, Zhifu Tao, Meng Yao, Yizhou Yao, Blair Fleet, Erik D. Goodman, John R. Deller

Vitreous Imaging System - A New Method for Medical Diagnosis 328

Boucherit Taieb

**SESSION: SOFTWARE PACKAGES AND OTHER COMPUTATIONAL TOPICS
IN BIOINFORMATICS + RELATED DISCUSSIONS**

A Network of Hidden Markov Models and its Analysis	337
<i>Liqing Zhang, Layne T Watson, Lenwood S. Heath</i>	
Correlation of Patristic Distance with Nominal Specimen Collection Date in Influenza A/H1N1 Neuraminidase-Encoding Segments	343
<i>Jack Horner</i>	
GAPDH Architecture at Low Guanidine Concentrations: First Derivative Analysis of the Descending Slope of the UV Absorbance Peak	350
<i>Jessica Kim, Christopher Theisen, Norbert Seidler</i>	
Instantiation and Adaptation of CRISP-DM to Bioinformatics Computational Processes	355
<i>Santiago Gonzalez, Victor Robles, Jose Maria Pena, Ernestina Menasalvas</i>	
Analysis of Metabolic Networks: On the Similarity of the Three Domains of Life	361
<i>Karl G Kugler, Laurin AJ Mueller, Matthias Dehmer</i>	
Construction and Analysis of Metabolite Network of Arabidopsis thaliana Pathways	367
<i>Kasthuribai Viswanathan, Nita Parekh</i>	
A Professional Science Master Degree in Health Informatics	373
<i>Kevin Daimi, Gregory Grabowski</i>	
Laterality of Motor Control before the Advent of Experimental Psychology: Revisiting David Kinnebrook's 'Error of Judgement' at Greenwich in 1796	379
<i>Iraj Derakhshan</i>	
 SESSION: COMPUTER-ASSISTED MEDICAL CARE + SERVICE SYSTEMS, DIAGNOSTIC TOOLS IN BIOMEDICAL, AND COMPUTER-BASED MEDICAL SYSTEMS 	
Diagnosis of Breast Cancer Using Averaged Proximity Measure between Samples	387
<i>Roman Andrushkiw, Ekaterina Golubeva, Dmytro Klyushin, Yuri Petunin, Natalya Boroday</i>	
An Extensible Software Architecture to Facilitate Disaster Response Planning	393
<i>Martin O'Neill II, Armin R. Mikler, Tamara Schneider</i>	
Computer Modeling of Diffuse Axonal Injury Mechanisms	401
<i>Igor Szczyrba, Martin Burtscher, Rafal Szczyrba</i>	
A Computational Linguistics Approach to the Identification of Biological Factors that Contribute to the Development and Progression of Lung Cancer	408
<i>Christopher Frenz, Cheng Luo, Egon Urgard, Andres Metspalu</i>	

The Living Experience of a Diabetic Adult in India Using Fuzzy Relational Maps (FRM) 412
Victor Devadoss Anthony Sany, Susanna Mystica Victor Devadoss

SleepGaze: A Wireless System for Monitoring and Detection of Sleep Disorders 418
K. A. Unnikrishna Menon, Davis Jose, Maneesha V. Ramesh

Doppler Ultrasound Blood Flow Measurement System for Assessing Coronary Revascularization 424
J Solano, M Fuentes, A Villar, J Prohias, F Garcia-Nocetti

Analysis of Electrogastragrams of the Elderly Subjects using Maximum Lyapunov Exponent - For the Evaluation of Motion Sickness induced by Stereoscopic Movies 429
Yasuyuki Matsuura, Masaru Miyao, Hiroki Takada

A Personalized Health Information System to Foster Preventive Medicine 434
Sebastian Klenk, Julia Mohrmann, Andre Burkovski, Jurgen Dippon, Peter Fritz, Gunther Heidemann

A High Throughput Computational Analysis of Claudin Gene Family in Human Ovarian Cancer 439
Shaukat Iqbal Malik, Sheema Sameen, Zoya Khalid

SESSION: DRUG TARGETS, IMMUNOTHERAPY, AND COMPUTATIONAL METHODS FOR SYSTEM + MICRO BIOLOGY

Classifying HIV-1 Circulating Recombinant Forms 447
Steven Eliuk, Keith Ruiter, Pierre Boulanger

Self-Regulating Physiologically Based Pharmacokinetic Model and Creation of Drug Concentration Profiles in Plasma and Tissues 454
Stanislav Polinkevych

Identifying Co-targets to Fight Drug Resistance Based on a Random Walk Model 461
Liang-Chun Chen, Hsiang-Yuan Yeh, Cheng-Yu Yeh, Carlos Roberto Arias, Von-Wun Soo

The Rhesus Macaque is Three Times as Diverse but More Closely Equivalent in 'Damaging' Coding Variation as Compared to the Human 468
Qiaoping Yuan, Zhifeng Zhou, Stephen G. Lindell, J. Dee Higley, Betsy Ferguson, Robert C. Thompson, Juan F. Lopez, Stephen J. Suomi, Basel Baghal, Maggie Baker, Deborah C. Mash, Christina S. Barr, David Goldman

The Peak of a Pandemic? - A Phylogenetic Analysis of the H1N1 Influenza Virus from 2009 to Present 477
Anthony Deeter, Mark Dalman, Gayathri Nimishakavi, Zhong-Hui Duan

Protease Complement of the Thermophilic Bacterium Coprothermobacter proteolyticus 484
Hong Cai, Jianying Gu, Yufeng Wang

Computational Analysis on Cuminum Cyminum Compounds Against Aldose Reductase as Anti-diabetic Agents 487
Naresh Babu Muppalaneni, Appa Rao Allam

Etiology of the Diseases Caused by Bacterium Escherichia Coli According to an Electromagnetic Mode 491
Juan Esteban Correa Lopez

SESSION: MODELLING, SIMULATION AND OPTIMIZATION OF BIOLOGICAL SYSTEMS

Multi-scale Modelling of the Bile Acid and Xenobiotic System 499
Noel Kennedy, Paul Thompson, Huiru Zheng, Werner Dubitzky

Computerized Platform for Optimal Organ Allocations in Kidney Exchanges 506
Yanhua Chen, Jack Kalbfleisch, Yijiang Li, Peter Song, Yan Zhou

Application of Bioinformatics Models to Define Influenza Virus A Subtypes 513
Mansour Ebrahimi, Parisa Agha-Golzadeh, Esmaeil Ebrahimie, N. Shamabadi

Simulated Docking of Oseltamivir with an Avian Influenza (A/H5N1) Neuraminidase Active Site 516
Jack Horner

Accelerate Numerical Diffusion Solver of 2D Multi-scale and Multi-resolution Agent-based Brain Cancer Model by Employing Graphics Processing Unit Technology 523
Beini Jiang, Le Zhang, Wen Zhang, Allan Struthers, Michael Berens, Xiaobo Zhou

EpiGraph: A Scalable Simulation Tool for Epidemiological Studies 529
Gonzalo Martín, Maria-Cristina Marinescu, David E. Singh, Jesús Carretero

Altered Gliclazide Metabolic Pathway and its Implications on Increased Therapeutic Response in CYP2C9*2: Molecular Dynamics Simulation and Autodock Studies 537
N Renuka, Hussaina Banu, Geetha Vasanthakumar

Optimizing a Cost Matrix to Solve Rare-Class Biological Problems 544
Mark J. Lawson, Lenwood S. Heath, Hai Zhao, Liqing Zhang

Flow and Particle Deposition Simulations with Heat-transfer in the Nine-generation Lung Airways 551
Bela Soni, Naveen Arra, Shahrouz Aliabadi

A Simple Nonadditive Model of Water 558
Gregory Wood

Modeling as a Tool for Controlling the Production of Biofuels: Ethanol from a Biomass 562
Aghareed M. Tayeb, N. A. Mostafa, I. A. Ashour

Analytical and Numerical Simulation of Epidemic Models using Maple and Sage 568
Veronica Orjuela Contreras

Simulating The Reconstruction of Metabolic Networks Using Maple 575
Diego Ignacio Vélez Jaramillo

Development of a Computing Mmodel for Resistance Screening of Citrus Limon Ccultivars Infected by the Ccausal Aagent of 'Mal secco' Phoma tracheiphila 581
Khaled Khanchouch, Mohamed R. Hajlaoui, Hakan Kutucu

SESSION: ALGEBRAIC BIOLOGY AND BIOINFORMATICS, ABB

The Genetic Code, 8-Dimensional Hypercomplex Numbers and Dyadic Shifts 589
Sergey Petoukhov

Alignment-free Phylogenetic Outline of a Random-sequence Library of Non-biological Proteins 596
Miguel Jimenez-Montano, Matthew He

Amino Acids, Euclidean Distance and Symmetric Matrix 603
Matthew He, Miguel Jimenez-Montano, Paolo Ricci

SESSION: PROTEIN STRUCTURE PROCESSING + MACHINE LEARNING + CLASSIFICATION + HPC + MODELING + GENOMICS + CLUSTERING + GENE REGULATORY NETWORKS + HEALTH INFORMATICS + MICROARRAY + BIOINFORMATICS + ASSISTIVE TECHNOLOGY + BIO-INSPIRED SYSTEMS + DATA ANALYSIS

SCOPE: An Open-Source, C++ Implementation for Calculation of Protein Energetics from First Principles 611
Timothy Matthew Fawcett, Stephanie Irausquin, Mikhail Simin, Homayoun Valafar

Comparative Study of Alternative Energy Functions for the HP Model of Protein Structure Prediction 618
Mario Garza-Fabre, Gregorio Toscano-Pulido, Eduardo Rodriguez-Tello

EST-PAC^{HPC} - a Web Portal for High-throughput EST Annotation and Protein Sequence Prediction 625
Adam Wong, Andrzej Goscinski, Christophe Lefevre

Collagen Type XI alpha-1 Chain Amino Propeptide Structural Model and Glycosaminoglycan Interactions in Silico	632
<i>Chris Mallory, Owen McDougal, Julia Oxford</i>	
Probability Density Profile Analysis: A Method for Identifying Novel Protein Structures	636
<i>Arjang Fahim, Stephanie Irausquin, Timothy Matthew Fawcett, Mikhail Simin, Homayoun Valafar</i>	
Mimicking Transcription Process to Recognise Promoters in E.coli	642
<i>Sobha Rani Timmappareddy</i>	
Bio-Medical Data Integration Based on MetaQuerier Architecture	648
<i>Khondker Hasan, Munirul Islam, M Samiullah Chowdhury, Eusuf Abdullah Mim, Naieem Khan</i>	
Expression Network Analysis of Abiotic Stress Responsive Myb in Rice	655
<i>Shuchi Smita, Amit Katiyar, Dev Mani Pandey, Viswanathan Chinnusamy, Kailash Chander Bansal</i>	
Simplifying Gene Expression Microarray Comparative Analysis	658
<i>Philip Church, Andrzej Goscinski, Adam Wong, Christophe Lefevre</i>	
Comparison of Affymetrix Expression Array Summarization Methods for Reproducibility and Consistency Across Studies	663
<i>Xiaoyang Ruan, Ourania Kosti, Rado Goldman, Hongfang Liu</i>	
Comprehensive Comparison of Gene Set Analysis Tools	670
<i>Zheng Liu, Xuejun Li, Yate-Ching Yuan, Xiwei Wu</i>	
High Performance Grid Computation of the Scattered Field Formulation for Nth Order Debye Modeling of the General Dispersive Media	674
<i>Haythm Abdallah, Hala Elsadek, Hesham Eldeeb, Nader Bagherzadeh</i>	
Criteria for Annihilation of HIV-1 During HAART Therapy	679
<i>Frank Nani, Mingxian Jin</i>	
Stochastic Modelling of Tumour Immune Interactions	686
<i>K. S. S. Iyer, Swaminathan Sankaran, Rahul Athale</i>	
A Gaussian Packing Model For Phasing in Macromolecular Crystallography	692
<i>Yan Yan, Gregory Chirikjian</i>	
Biological Data Handling Methods	699
<i>Pradeep Achan, Ajit Warriar, Bhadrachalam Chitturi</i>	

A Bioinformatics Approach for Identification of Type III Signal Anchored Proteins in Rice	706
<i>Amit Katiyar, Shuchi Smita, Dev Mani Pandey, Viswanathan Chinnusamy, Kailash Chander Bansal</i>	
Application of W-curves and TSP to Clustering HIV1 Sequences	710
<i>Doug Cork, Steven Lembark, Nelson Michael, Jerome Kim</i>	
Electronic Health Records and Mobile Technology Use in Northwest Florida Medical Practices	716
<i>Edward Rodgers</i>	
Anode Effects on Microbial Fuel Cell Efficiency	718
<i>Michaela Brant, Geoffrey Chu, Mark Claire, Jane Curnutt, Ernesto Gomez, Andrea Gonzalez, Carly Gott, Michael Grigsby, Ruben Hovanesian, George Kaladjian, Jena Losch, Alex Nguyen, Alexandra Olano, Geoffrey Payton, Amina Razzak, Kara Rotunno, Sarah Saleemi, Allison Scheppelmann, Keith Schubert, Gerardo Solis, Elizabeth Statmore, Kristin Symer</i>	
Emerging Viral Agents at Risk in Global Health Approaches to Early Diagnosis and Prompt Therapy	722
<i>Giulio Tarro, Ciro Esposito</i>	
Applications of Artificial Immune Systems	726
<i>Suhair Amer</i>	
On a Body Sway Model while Maintaining Upright Posture during Exposure to a Stereoscopic Movie on a Liquid Crystal Display	731
<i>Hiroki Takada, Kazuhiro Fujikake, Masaru Miyao</i>	
An Assistive Technology Computer Control System	738
<i>Eduardo Alberti, Tatiany Kazmieczech, Alessandro Brawerman</i>	
A Proposal of a Comprehensive Medical Emergency Decision Support System	744
<i>Asma AlJarullah, Samir El-Masri</i>	
Uncertain Gene Regulatory Networks Simplified by Gramian-Based Approach	751
<i>Anke Meyer-Baese, Susanne Cappendijk, Fabian Theis</i>	
Proposal of a Web Based Ambulance System in Saudi Arabia	760
<i>Hebah Mirza, Samir El-Masri</i>	
Stability Analysis of Hybrid Stochastic Gene Regulatory Networks	767
<i>Anke Meyer-Baese, Claudia Plant, Jan Krumsiek, Fabian Theis, Marc R. Emmett, Charles A. Conrad</i>	

Towards Integrating National Electronic Care Records in Saudi Arabia	777
<i>Mohammed Alnuem, Samir El-Masri, Ahmed Youssef, Ahmed Emam</i>	
Dynamics of HIV-1 Associated Kaposi Sarcoma During HAART Therapy	783
<i>Frank Nani, Mingxian Jin</i>	
A Proposal of Clinical Decision Support system Architecture for Distributed Electronic Health Records	787
<i>Shaker El-Sappagh, Samir El-Masri</i>	
Simulation of Genetic Regulatory Networks	794
<i>Rafat Parveen</i>	
TTCS: Three-Dimensional and Two-Dimensional Compound Structure Search Online Tools	800
<i>Hongzhi Li, Haiqing Li, Edward Lee, Yate-Ching Yuan</i>	
Cyberinfrastructure: A Case Study of IT Infrastructure for Next Generation Bioinformatics and Computational Biology	802
<i>Haiqing Li, Yate-Ching Yuan</i>	